



SEQUENCE LISTING

<110> Arthur B. Raitano
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 Mary Faris
 Rene S. Hubert
 Steve Chappell Mitchell
 Douglas C. Saffran

<120> NOVEL G PROTEIN-COUPLED RECEPTOR
 UP-REGULATED IN PROSTATE CANCER AND USES THEREOF

<130> 511582002410

<140> US 10/017,066
<141> 2001-12-14

<150> US 09/680,728
<150> 2000-10-05

<150> 60/157,902
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agttcttca tg atg gtt gat ccc aat ggc aat gaa tcc agt gct aca tac 171
Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr

1	5	10
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ttc atc cta ata ggc ctc cct ggt tta gaa gag gct cag ttc tgg ttg 219
Phe Ile Leu Ile Gly Leu Pro Gly Leu Glu Ala Gln Phe Trp Leu
15 20 25

gcc ttc cca ttg tgc tcc ctc tac ctt att gct gtt cta ggt aac ttg 267
Ala Phe Pro Leu Cys Ser Leu Tyr Ile Ala Val Leu Gly Asn Leu
30 35 40 45

aca atc atc tac att gtt cgg act gag cac agc ctg cat gag ccc atg 315
Thr Ile Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met
50 55 60

tat ata ttt ctt tgc atg ct't tca' ggc att gac atc ctc atc tcc acc Tyr Ile Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr	65	70	75	363
tca tcc atg ccc aaa atg ctg gcc atc ttc tgg ttc aat tcc act acc Ser Ser Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr	80	85	90	411
atc cag ttt gat gct tgt ctg cta cag att ttt gcc atc cac tcc tta Ile Gln Phe Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu	95	100	105	459
tct ggc atg gaa tcc aca gtg ctg ctg gcc atg gct ttt gac cgc tat Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr	110	115	120	507
gtg gcc atc tgt cac cca ctg cgc cat gcc aca gta ctt acg ttg cct Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro	130	135	140	555
cgt gtc acc aaa att ggt gtg gct gtc gtg gtg cgg ggg gct gca ctg Arg Val Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu	145	150	155	603
atg gca ccc ctt cct gtc ttc atc aag cag ctg ccc ttc tgc cgc tcc Met Ala Pro Ile Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser	160	165	170	651
aat atc ctt tcc cat tcc tac tgc cta cac caa gat gtc atg aag ctg Asn Ile Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu	175	180	185	699
gcc tgt gat gat atc cgg gtc aat gtc gtc tat ggc ctt atc gtc atc Ala Cys Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile	190	195	200	747
atc tcc gcc att ggc ctg gac tca ctt ctc atc tcc ttc tca tat ctg Ile Ser Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu	210	215	220	795
ctt att ctt aag act gtg ttg ggc ttg aca cgt gaa gcc cag gcc aag Leu Ile Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys	225	230	235	843
gca ttt ggc act tgc gtc tct cat gtg tgt gct gtg ttc ata ttc tat Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr	240	245	250	891
gta cct ttc att gga ttg tcc atg gtg cat cgc ttt agc aag cgg cgt Val Pro Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg	255	260	265	939
gac tct ccg ctg ccc gtc atc ttg gcc aat atc tat ctg ctg gtt cct Asp Ser Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro	270	275	280	987
cct gtg ctc aac cca att gtc tat gga gtg aag aca aag gag att cga				1035

Pro Val Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg		
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Gln Arg Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro		
305	310	315
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ccttcaaata tggaaactggg tggggaatct ccatttttc aatattattt tcttcttgg	1263	
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Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile Ile
      35          40          45
Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
      50          55          60

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Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser Met
 65 70 75 80
 Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe
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 Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu Ser Gly Met
 100 105 110
 Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr
 130 135 140
 Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala Pro
 145 150 155 160
 Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp
 180 185 190
 Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser Ala
 195 200 205
 Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile Leu
 210 215 220
 Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe Gly
 225 230 235 240
 Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro Phe
 245 250 255
 Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro
 260 265 270
 Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val Leu
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 Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
 35 40 45
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50 55 60
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
 65 70 75 80
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
 85 90 95
 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 100 105 110
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
 130 135 140

Met Val Ala Leu Val Arg Gly Ser' Leu Phe Phe Pro Leu Pro Leu
 145 150 155 160
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
 180 185 190
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
 210 215 220
 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
 245 250 255
 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
 260 265 270
 Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
 275 280 285
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 Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
 305 310 315 320

<210> 4
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 <213> Homo Sapiens

<400> 4

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 35 40 45
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50 55 60
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 65 70 75 80
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Ile Glu Ala Cys
 85 90 95
 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 100 105 110
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
 130 135 140
 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu
 145 150 155 160
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
 180 185 190
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
 210 215 220

Leu	Gln	Leu	Pro	Ser	Lys	Sér	Glu	Arg	Ala	Lys	Ala	Phe	Gly	Thr	Cys
225							230					235			240
Val	Ser	His	Ile	Gly	Val	Val	Leu	Ala	Phe	Tyr	Val	Pro	Leu	Ile	Gly
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Leu	Ser	Val	Val	His	Arg	Phe	Gly	Asn	Ser	Leu	His	Pro	Ile	Val	Arg
						260			265			270			
Val	Val	Met	Gly	Asp	Ile	Tyr	Leu	Leu	Leu	Pro	Pro	Val	Ile	Asn	Pro
						275			280			285			
Ile	Ile	Tyr	Gly	Ala	Lys	Thr	Lys	Gln	Ile	Arg	Thr	Arg	Val	Leu	Ala
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aaactggttgc	ggaatctcc	atttttcaa	tattatttc	ttctttgttt	tcttgctacg										180
tataattttt	aatatcctga	ctaggttgt	gttggagggt	tattactttt	cattttacca										240
tgcagttccaa	atctaaactg	cttctactga	tggtttacag	cattctgaga	taagaatgg										300
acatcttagag	aacatttgcc	aaaggcctaa	gcacagcaa	ggaaaataaa	cacagaatat										360
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tct	tat	atc	ttt	atc	ctt	cag	gca	gtt	cta	caa	ctc	tcc	tct	cag	gag
Ser	Tyr	Ile	Phe	Ile	Leu	Gln	Ala	Val	Leu	Gln	Leu	Ser	Ser	Gln	Glu
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20									25						30

gcc	cgc	tac	aaa	gca	ttt	ggg	aca	tgt	gtc	tct	cac	ata	ggt	gcc	atc
Ala	Arg	Tyr	Lys	Ala	Phe	Gly	Thr	Cys	Val	Ser	His	Ile	Gly	Ala	Ile
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35									40						45

tta	gcc	ttc	tac	aca	cct	tca	gtc	atc	tct	tca	gtc	atg	cac	cgt	gtg
Leu	Ala	Phe	Tyr	Thr	Pro	Ser	Val	Ile	Ser	Ser	Val	Met	His	Arg	Val
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50								55				60			

gcc	cgc	tgt	gtg	cca	cac	gtc	cac	att	ctc	ctc	gcc	aat	ttc	tat	
Ala	Arg	Cys	Ala	Val	Pro	His	Val	His	Ile	Leu	Ala	Asn	Phe	Tyr	
									75						240
65															80

ctg ctc ttc cca ccc atg gtc aat ccc atc atc tat ggc gtt aag acc	288
Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile Tyr Gly Val Lys Thr	
85 90 95	
aag cag atc cgt gac agt ctt ggg agt att cct gag aaa gga tgt gtg	336
Lys Gln Ile Arg Asp Ser Leu Gly Ser Ile Pro Glu Lys Gly Cys Val	
100 105 110	
aat aga gag tga gga ata agt gga aaa aga gtg ggg ccc agt gaa tgc	384
Asn Arg Glu * Gly Ile Ser Gly Lys Arg Val Gly Pro Ser Glu Cys	
115 120 125	
tgt agt ggg cca ggg ctg tgc tga gag tag atg ggt cct aga ctc cac	432
Cys Ser Gly Pro Gly Leu Cys * Glu * Met Gly Pro Arg Leu His	
130 135 140	
gtt tag ttc ttt tct tgt att atg aaa aga ata aat gat gtc ctg aag	480
Val * Phe Phe Ser Cys Ile Met Lys Arg Ile Asn Asp Val Leu Lys	
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 Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser His Ile Gly Ala Ile
 35 40 45
 Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser Val Met His Arg Val
 50 55 60
 Ala Arg Cys Ala Val Pro His Val His Ile Leu Ala Asn Phe Tyr
 65 70 75 80
 Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile Tyr Gly Val Lys Thr
 85 90 95
 Lys Gln Ile Arg Asp Ser Leu Gly Ser Ile Pro Glu Lys Gly Cys Val
 100 105 110
 Asn Arg Glu Gly Ile Ser Gly Lys Arg Val Gly Pro Ser Glu Cys Cys
 115 120 125
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